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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/612,925D

DATE: 03/19/2003
TIME: 11:57:41

Input Set : **N:\Crf3\RULE60\09612925.raw.txt**
Output Set: **N:\CRF4\03192003\I612925D.raw**

SEQUENCE LISTING
3 (1) GENERAL INFORMATION:
5   (i) APPLICANT: DUARTE CANO, C. A.
6   GUILL N NIETO, G. E.
7   MART N DUNN, A. M.
8   ALVAREZ ACOSTA, A.
9   CARPIO MU%OZ, E. L.
10.   QUINTANA V. D.
11   G MEZ RODR GUEZ, C. E.
12   SILVA RODR GUEZ, R. C.
13   NAZ BAL G LVEZ, C.
14   LEAL ANGULO, M. J.
16   (ii) TITLE OF INVENTION: System for the expression of heterologous
17   antigens as fusion proteins
19 (iii) NUMBER OF SEQUENCES: 21
21   (iv) CORRESPONDENCE ADDRESS:
22   (A) ADDRESSEE: Lackenbach Siegel Marzullo Aronson & Greenspan
23   (B) STREET: One Chase Road
24   (C) CITY: Scarsdale
25   (D) STATE: New York
26   (E) COUNTRY: U.S.
27   (F) ZIP: 10583
29   (v) COMPUTER READABLE FORM:
30   (A) MEDIUM TYPE: Floppy disk 3.5'' (1.4 MB).
31   (B) COMPUTER: Compatible PC IBM (80486, 8 M Ram).
32   (C) OPERATING SYSTEM: Windows 95.
33   (D) SOFTWARE: Word Perfect 5.0 for Windows 95.
35   (vi) CURRENT APPLICATION DATA:
C--> 36   **(A) APPLICATION NUMBER: US/09/612,925D**
C--> 37   **(B) FILING DATE: 10-Jul-2000**
W--> 43   **(C) CLASSIFICATION: 435**
40 (vii) PRIOR APPLICATION DATA:
41   (A) APPLICATION NUMBER: US/08/930,917A
42   (B) FILING DATE: 16-Sep-1997
44   (A) APPLICATION NUMBER: PCT/CU97/00001
45   (B) FILING DATE: 17-Jan-1997
47 (viii) ATTORNEY/AGENT INFORMATION:
48   (A) NAME: HENRY A. MARZULLO, JR.
49   (B) REGISTRATION NUMBER: 20,910
50   (C) REFERENCE/DOCKET NUMBER: P-13
52   (ix) TELECOMMUNICATION INFORMATION:
53   (A) TELEPHONE: (914) 723-4300
54   (B) TELEFAX: (914) 723-4301

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Input Set : **N:\Crf3\RULE60\09612925.raw.txt**
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```
57 (2) INFORMATION FOR SEQ ID NO: 1:
59       (i) SEQUENCE CHARACTERISTICS:
60           (A) LENGTH: 47 Amino acid residues
61           (B) TYPE: Amino acid
62           (C) STRANDEDNESS: Unknown
63           (D) TOPOLOGY: Unknown
65      (ii) MOLECULE TYPE: Peptide
67     (iii) HYPOTHETICAL: No
69      (iv) ANTI-SENSE: No
W--> 71      (v) FRAGMENT TYPE: -N Terminal fragment
73      (vi) ORIGINAL SOURCE:
74           (A) ORGANISM: Neisseria meningitidis
75           (B) STRAIN: B:4:P1.15
77     (vii) IMMEDIATE SOURCE:
78           (A) LIBRARY: Genomic
79           (B) CLONE: P64K
81.     (ix) FEATURE:
82           (D) OTHER INFORMATION: First 47 amino acids of the recombinant protein
83 of Neisseria meningitidis P64K.
85      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
86 Met Leu Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile
87 1               5                   10                  15
88 Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly
89              20                  25                  30
90 Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Glu Thr Asp
91          35                  40                  45
93 (2) INFORMATION FOR SEQ ID NO: 2:
94       (i) SEQUENCE CHARACTERISTICS:
95           (A) LENGTH: 29 base pairs
96           (B) TYPE: Nucleic acid
97           (C) STRANDEDNESS: Unknown
98           (D) TOPOLOGY: Unknown
100     (ii) MOLECULE TYPE: Other nucleic acid
101          (A) DESCRIPTION: Synthetic oligonucleotide
103    (iii) HYPOTHETICAL: No.
105     (iv) ANTI-SENSE: No
W--> 107     (v) FRAGMENT TYPE: -N Terminal fragment
109     (vi) ORIGINAL SOURCE:
110          (A) ORGANISM: Neisseria meningitidis
111          (B) STRAIN: B:4:P1.15
113    (vii) IMMEDIATE SOURCE:
114          (A) LIBRARY: Genomic
115          (B) CLONE: P64K
117     (ix) FEATURE:
118          (A) NAME/KEY: 1573
119          (D) OTHER INFORMATION: Primer 5' for PCR amplification of the first
120 44 amino acids of the recombinant protein of Neisseria
121 meningitidis P64K.
123     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
```

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```
        124
TTCCATGGTA   GATAAAAGAA   TGGCTTTAG                                    29
        126 (2)  INFORMATION FOR SEQ ID NO: 3:
        128      (i)  SEQUENCE CHARACTERISTICS:
        129           (A) LENGTH: 29 base pairs
        130           (B) TYPE: Nucleic acid
        131           (C) STRANDEDNESS: Unknown
        132           (D) TOPOLOGY: Unknown
        134     (ii)  MOLECULE TYPE: Other nucleic acid
        135           (A) DESCRIPTION: Synthetic oligonucleotide
        137    (iii)  HYPOTHETICAL: No.
        139     (iv)  ANTI-SENSE: No
W--> 141      (v)  FRAGMENT TYPE: -C Terminal fragment
        142     (vi)  ORIGINAL SOURCE:
        143           (A) ORGANISM: Neisseria meningitidis
        144           (B) STRAIN: B:4:P1.15
        146    (vii)  IMMEDIATE SOURCE:
        147           (A) LIBRARY: Genomic
        148           (B) CLONE: P64K
        150     (ix)  FEATURE:
        151           (A) NAME/KEY: 1575
        152           (D) OTHER INFORMATION: Primer 3' for PCR amplification of the first
        153 47 amino acids of the recombinant protein of Neisseria
        154 meningitidis P64K.
        156      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
        157 TTTCTAGATC   CAAAGTAATC   AGGGTATCG                         29
        159 (2) INFORMATION FOR SEQ ID NO: 4:
        161      (i)  SEQUENCE CHARACTERISTICS:
        162           (A) LENGTH: 26 base pairs
        163           (B) TYPE: Nucleic acid
        164           (C) STRANDEDNESS: Unknown
        165           (D) TOPOLOGY: Unknown
        167     (ii) MOLECULE TYPE: Other nucleic acid
        168           (A) DESCRIPTION: Synthetic oligonucleotide
        170    (iii) HYPOTHETICAL: No
        172     (iv) ANTI-SENSE: No
W--> 174      (v)  FRAGMENT TYPE: -C Terminal fragment
        176     (vi) ORIGINAL SOURCE:
        177           (A) ORGANISM: Neisseria meningitidis
        178           (B) STRAIN: B:4:P1.15
        180    (vii) IMMEDIATE SOURCE:
        181           (A) LIBRARY: Genomic
        182           (B) CLONE: P64K
        184     (ix) FEATURE:
        185           (A) NAME/KEY: Primer 2192
        186           (D) OTHER INFORMATION: Primer 3' for PCR amplification of the first
        187 120 amino acids of the recombinant protein of Neisseria
        188 meningitidis P64K
        190      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
        191  GGCGGTTCTG   CCGATTAAGG   ATCCGA                           26
```

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Input Set : **N:\Crf3\RULE60\09612925.raw.txt**
Output Set: **N:\CRF4\03192003\I612925D.raw**

```
193 (2) INFORMATION FOR SEQ ID NO: 5:
195      (i) SEQUENCE CHARACTERISTICS:
196          (A) LENGTH: 146 base pairs
197          (B) TYPE: Nucleic acid
198          (C) STRANDEDNESS: Unknown
199          (D) TOPOLOGY: Unknown
201     (ii) MOLECULE TYPE: Other nucleic acid
202          (A) DESCRIPTION: Fragment amplified by PCR
204    (iii) HYPOTHETICAL: Yes
206     (iv) ANTI-SENSE: No
208      (v) FRAGMENT TYPE: -N-terminal fragment
210     (vi) ORIGINAL SOURCE:
211          (A) ORGANISM: Neisseria meningitidis
212          (B) STRAIN: B:4:P1.15
214    (vii) IMMEDIATE SOURCE:
215          (A) LIBRARY: Genomic
216          (B) CLONE: P64K
218     (ix) FEATURE:
219          (D) OTHER INFORMATION: Fragment derived from the first 47 amino acids
220 of the recombinant protein of Neisseria meningitidis P64K,
221 containing a NcoI site at the position 3 to 8 and a XbaI site
222 at the position 139 to 144
224     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
225 TTCCATGGTA   GATAAAGAA   TGGCTTTAGT   TGAATTGAAA   GTGCCCGACA   TTGGCGGACA    60
227 CGAAAATGTA   GATATTATCG   CGGTTGAAGT   AAACGTGGGC   GACACTATTG   CTGTGGACGA   120
229 TACCCTGATT   ACTTTGGATC   TAGAAA                                            146
232 (2) INFORMATION FOR SEQ ID NO: 6:
234      (i) SEQUENCE CHARACTERISTICS:
235          (A) LENGTH: 47 Amino acid residues
236          (B) TYPE: Amino acid
237          (C) STRANDEDNESS: Unknown
238          (D) TOPOLOGY: Unknown
240     (ii) MOLECULE TYPE: Peptide
242    (iii) HYPOTHETICAL: No
244     (iv) ANTI-SENSE: No
```
W--> **246   (v) FRAGMENT TYPE: -N Terminal fragment**
```
248     (vi) ORIGINAL SOURCE:
249          (A) ORGANISM: Neisseria meningitidis
250          (B) STRAIN: B:4:P1.15
252    (vii) IMMEDIATE SOURCE:
253          (A) LIBRARY: Genomic
254          (B) CLONE: P64K
256     (ix) FEATURE:
257          (D) OTHER INFORMATION: Stabilizer derived from the first 47 amino
258 acids of the recombinant protein of Neisseria meningitidis P64K,
259 containing the following changes: L2 V2; E45 D45;T46 L46; D47 E47.
261     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
262 Met Val Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile
263 1               5                   10                  15
```

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Output Set: N:\CRF4\03192003\I612925D.raw

```
264 Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly
265             20                  25                  30
266 Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Asp Leu Glu
267         35                  40                  45
269 (2) INFORMATION FOR SEQ ID NO: 7:
271     (i) SEQUENCE CHARACTERISTICS:
272             (A) LENGTH: 16 base pairs
273             (B) TYPE: Nucleic acid
274             (C) STRANDEDNESS: Unknown
275             (D) TOPOLOGY: Unknown
276     (ii) MOLECULE TYPE: Other nucleic acid
277             (A) DESCRIPTION: Synthetic oligonucleotide
279     (iii) HYPOTHETICAL: No.
281     (iv) ANTI-SENSE: No
W--> 283     (v) FRAGMENT TYPE: -N Terminal fragment
285     (vi) ORIGINAL SOURCE:
286             (A) ORGANISM: Neisseria meningitidis
287             (B) STRAIN: B:4:P1.15
289     (vii) IMMEDIATE SOURCE:
290             (A) LIBRARY: Genomic
291             (B) CLONE: P64K
293     (ix) FEATURE:
294             (A) NAME/KEY: 1576
295     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
296 CTAGATTTGA   TATCAG                                       16
298 (2) INFORMATION FOR SEQ ID NO: 8:
300     (i) SEQUENCE CHARACTERISTICS:
301             (A) LENGTH: 16 base pairs
302             (B) TYPE: Nucleic acid
303             (C) STRANDEDNESS: Unknown
304             (D) TOPOLOGY: Unknown
306     (ii) MOLECULE TYPE: Other nucleic acid
307             (A) DESCRIPTION: Synthetic oligonucleotide
309     (iii) HYPOTHETICAL: No
311     (iv) ANTI-SENSE: No
W--> 313     (v) FRAGMENT TYPE: -N Terminal fragment
315     (vi) ORIGINAL SOURCE:
316             (A) ORGANISM: Neisseria meningitidis
317             (B) STRAIN: B:4:P1.15
319     (vii) IMMEDIATE SOURCE:
320             (A) LIBRARY: Genomic
321             (B) CLONE: P64K
323     (ix) FEATURE:
324             (A) NAME/KEY: 1577
326     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8 :
327 GATCCTGATA   TCAAAT                                       16
329 (2) INFORMATION FOR SEQ ID NO: 9:
331     (i) SEQUENCE CHARACTERISTICS:
332             (A) LENGTH: 15 Amino acid residues
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/19/2003
PATENT APPLICATION: **US/09/612,925D**   TIME: 11:57:42

Input Set : **N:\Crf3\RULE60\09612925.raw.txt**
Output Set: **N:\CRF4\03192003\I612925D.raw**

<u>Invalid Line Length</u>:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2; Line(s) 124
Seq#:5; Line(s) 225,227
Seq#:21; Line(s) 739,741,745,747,749

VERIFICATION SUMMARY   DATE: 03/19/2003
PATENT APPLICATION: **US/09/612,925D**   TIME: 11:57:42

Input Set : **N:\Crf3\RULE60\09612925.raw.txt**
Output Set: **N:\CRF4\03192003\I612925D.raw**

L:36 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:37 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:43 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:71 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=1
L:107 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=2
L:141 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=3
L:174 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=4
L:246 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=6
L:283 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=7
L:313 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=8
L:571 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:571 M:238 W: Alpha Fields not Ordered, Reordered [(D) TOPOLOGY:] of (2)(i)
L:571 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=17
L:571 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=17
L:598 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:598 M:238 W: Alpha Fields not Ordered, Reordered [(D) TOPOLOGY:] of (2)(i)
L:598 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=18
L:598 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=18
L:640 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:640 M:238 W: Alpha Fields not Ordered, Reordered [(D) TOPOLOGY:] of (2)(i)
L:640 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=19
L:640 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=19
L:685 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:685 M:238 W: Alpha Fields not Ordered, Reordered [(D) TOPOLOGY:] of (2)(i)
L:685 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=20
L:685 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=20
L:734 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:734 M:238 W: Alpha Fields not Ordered, Reordered [(D) TOPOLOGY:] of (2)(i)
L:734 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=21
L:734 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=21